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1645

TECH CENTER 1600/2900



## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/724,586

DATE: 09/04/2002

TIME: 11:57:34

Input Set : N:\Crf3\RULE60\09724586.raw  
 Output Set: N:\CRF4\09042002\I724586.raw

PFF

1 <110> APPLICANT: Sakowicz, Roman  
 2 Goldstein, Lawrence S. B.  
 3 The Regents of the University of California  
 4 <120> TITLE OF INVENTION: Identification and Expression of a Novel Kinesin Motor  
 5 Protein  
 6 <130> FILE REFERENCE: 18557C-000710US  
 7 <140> CURRENT APPLICATION NUMBER: 09/724,586  
 8 <141> CURRENT FILING DATE: 2000-11-28  
 10 <150> PRIOR APPLICATION NUMBER: US/09/235,416  
 11 <151> PRIOR FILING DATE: 1999-01-22  
 14 <150> PRIOR APPLICATION NUMBER: WO PCT/US99/01355  
 15 <151> PRIOR FILING DATE: 1999-01-22  
 16 <150> PRIOR APPLICATION NUMBER: US 60/072,361  
 17 <151> PRIOR FILING DATE: 1998-01-23  
 18 <160> NUMBER OF SEQ ID NOS: 7  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 784  
 23 <212> TYPE: PRT  
 24 <213> ORGANISM: Thermomyces lanuginosus  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed  
 27 microtubule motor protein  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: DOMAIN  
 30 <222> LOCATION: (1)..(357)  
 31 <223> OTHER INFORMATION: kinesin-like microtubule motor domain  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: DOMAIN  
 34 <222> LOCATION: (358)..(442)  
 35 <223> OTHER INFORMATION: neck domain links motor domain to stalk domain  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: DOMAIN  
 38 <222> LOCATION: (443)..(601)  
 39 <223> OTHER INFORMATION: stalk domain, unc-104 family domain  
 40 <220> FEATURE:  
 41 <221> NAME/KEY: DOMAIN  
 42 <222> LOCATION: (602)..(784)  
 43 <223> OTHER INFORMATION: tail domain  
 44 <400> SEQUENCE: 1  
 45 Met Ser Gly Gly Asn Ile Lys Val Val Val Arg Val Arg Pro Phe  
 46 1 5 10 15  
 47 Asn Ala Arg Glu Ile Asp Arg Gly Ala Lys Cys Ile Val Arg Met Glu

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48	20	25	30
49	Gly Asn Gln Thr Ile Leu Thr Pro Pro Pro Gly Ala Glu Glu Lys Ala		
50	35	40	45
51	Arg Lys Ser Gly Lys Thr Ile Met Asp Gly Pro Lys Ala Phe Ala Phe		
52	50	55	60
53	Asp Arg Ser Tyr Trp Ser Phe Asp Lys Asn Ala Pro Asn Tyr Ala Arg		
54	65	70	75
55	Gln Glu Asp Leu Phe Gln Asp Leu Gly Val Pro Leu Leu Asp Asn Ala		
56	85	90	95
57	Phe Lys Gly Tyr Asn Asn Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser		
58	100	105	110
59	Gly Lys Ser Tyr Ser Met Met Gly Tyr Gly Lys Glu His Gly Val Ile		
60	115	120	125
61	Pro Arg Ile Cys Gln Asp Met Phe Arg Arg Ile Asn Glu Leu Gln Lys		
62	130	135	140
63	Asp Lys Asn Leu Thr Cys Thr Val Glu Val Ser Tyr Leu Glu Ile Tyr		
64	145	150	155
65	Asn Glu Arg Val Arg Asp Leu Leu Asn Pro Ser Thr Lys Gly Asn Leu		
66	165	170	175
67	Lys Val Arg Glu His Pro Ser Thr Gly Pro Tyr Val Glu Asp Leu Ala		
68	180	185	190
69	Lys Leu Val Val Arg Ser Phe Gln Glu Ile Glu Asn Leu Met Asp Glu		
70	195	200	205
71	Gly Asn Lys Ala Arg Thr Val Ala Ala Thr Asn Met Asn Glu Thr Ser		
72	210	215	220
73	Ser Arg Ser His Ala Val Phe Thr Leu Thr Leu Thr Gln Lys Trp His		
74	225	230	235
75	Asp Glu Glu Thr Lys Met Asp Thr Glu Lys Val Ala Lys Ile Ser Leu		
76	245	250	255
77	Val Asp Leu Ala Gly Ser Glu Arg Ala Thr Ser Thr Gly Ala Thr Gly		
78	260	265	270
79	Ala Arg Leu Lys Glu Gly Ala Glu Ile Asn Arg Ser Leu Ser Thr Leu		
80	275	280	285
81	Gly Arg Val Ile Ala Ala Leu Ala Asp Met Ser Ser Gly Lys Gln Lys		
82	290	295	300
83	Lys Asn Gln Leu Val Pro Tyr Arg Asp Ser Val Leu Thr Trp Leu Leu		
84	305	310	315
85	320		
86	Lys Asp Ser Leu Gly Gly Asn Ser Met Thr Ala Met Ile Ala Ala Ile		
87	325	330	335
88	Ser Pro Ala Asp Ile Asn Phe Glu Glu Thr Leu Ser Thr Leu Arg Tyr		
89	340	345	350
90	Ala Asp Ser Ala Lys Arg Ile Lys Asn His Ala Val Val Asn Glu Asp		
91	355	360	365
92	Pro Asn Ala Arg Met Ile Arg Glu Leu Lys Glu Glu Leu Ala Gln Leu		
93	370	375	380
94	Arg Ser Lys Leu Gln Ser Ser Gly Gly Gly Gly Gly Ala Gly Gly		
95	385	390	395
96	Ser Gly Gly Pro Val Glu Glu Ser Tyr Pro Pro Asp Thr Pro Leu Glu		
	405	410	415

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97 Lys Gln Ile Val Ser Ile Gln Gln Pro Asp Ala Thr Val Lys Lys Met  
 98 420 425 430  
 99 Ser Lys Ala Glu Ile Val Glu Gln Leu Asn Gln Ser Glu Lys Leu Tyr  
 100 435 440 445  
 101 Arg Asp Leu Asn Gln Thr Trp Glu Glu Lys Leu Ala Lys Thr Glu Glu  
 102 450 455 460  
 103 Ile His Lys Glu Arg Glu Ala Ala Leu Glu Glu Leu Gly Ile Ser Ile  
 104 465 470 475 480  
 105 Glu Lys Gly Phe Val Gly Pro Tyr His Ser Lys Glu Met Pro His Leu  
 106 485 490 495  
 107 Val Asn Leu Ser Asp Asp Pro Leu Leu Ala Glu Cys Leu Val Tyr Asn  
 108 500 505 510  
 109 Ile Lys Pro Gly Gln Thr Arg Val Gly Asn Val Asn Gln Asp Thr Gln  
 110 515 520 525  
 111 Ala Glu Ile Arg Leu Asn Gly Ser Lys Ile Leu Lys Glu His Cys Thr  
 112 530 535 540  
 113 Phe Glu Asn Val Asp Asn Val Val Thr Ile Val Pro Asn Glu Lys Ala  
 114 545 550 555 560  
 115 Ala Val Met Val Asn Gly Val Arg Ile Asp Lys Pro Thr Arg Leu Arg  
 116 565 570 575  
 117 Ser Gly Tyr Arg Ile Ile Leu Gly Asp Phe His Ile Phe Arg Phe Asn  
 118 580 585 590  
 119 His Pro Glu Glu Ala Arg Ala Glu Arg Gln Glu Gln Ser Leu Leu Arg  
 120 595 600 605  
 121 His Ser Val Thr Asn Ser Gln Leu Gly Ser Pro Ala Pro Gly Arg His  
 122 610 615 620  
 123 Asp Arg Thr Leu Ser Lys Ala Gly Ser Asp Ala Asp Gly Asp Ser Arg  
 124 625 630 635 640  
 125 Ser Asp Ser Pro Leu Pro His Phe Arg Gly Lys Asp Ser Asp Trp Phe  
 126 645 650 655  
 127 Tyr Ala Arg Arg Glu Ala Ala Ser Ala Ile Leu Gly Leu Asp Gln Lys  
 128 660 665 670  
 129 Ile Ser His Leu Thr Asp Asp Glu Leu Asp Ala Leu Phe Asp Asp Val  
 130 675 680 685  
 131 Gln Lys Ala Arg Ala Val Arg Arg Gly Leu Val Glu Asp Asn Glu Asp  
 132 690 695 700  
 133 Ser Asp Ser Gln Ser Ser Phe Pro Val Arg Asp Lys Tyr Met Ser Asn  
 134 705 710 715 720  
 135 Gly Thr Ile Asp Asn Phe Ser Leu Asp Thr Ala Ile Thr Met Pro Gly  
 136 725 730 735  
 137 Thr Pro Arg Ser Asp Asp Gly Asp Ala Leu Phe Phe Gly Asp Lys  
 138 740 745 750  
 139 Lys Ser Lys Gln Asp Ala Ser Asn Val Asp Val Glu Glu Leu Arg Gln  
 140 755 760 765  
 141 Gln Gln Ala Gln Met Glu Glu Ala Leu Lys Thr Ala Lys Gln Glu Phe  
 142 770 775 780  
 144 <210> SEQ ID NO: 2  
 145 <211> LENGTH: 2352  
 146 <212> TYPE: DNA

RAW SEQUENCE LISTING  
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Output Set: N:\CRF4\09042002\I724586.raw

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147 <213> ORGANISM: Thermomyces lanuginosus
148 <220> FEATURE:
149 <223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed
150 microtubule motor protein
151 <400> SEQUENCE: 2
152 atgtcggcg gtggaaatat caaggtggtg gtgcgggtac gcccgttcaa cgcccgagaa 60
153 atcgaccgtg gcgc当地at tattgtgcgg atggaaggaa atcaaaccat cctcaccct 120
154 cctccgggtg cc当地agagaa ggc当地gtaaa agtggcaaaa ctattatgta tggccc当地ag 180
155 gc当地ttgcgt tc当地atcggtc gtattggtcc tttgacaaga atgctccaa ctatgc当地gaga 240
156 caggaagacc tattccaaga tctcggagtc cc当地tctctgg ataatgcatt caagggttat 300
157 aacaattgttata tcttc当地cta cc当地tccagacc ggttccggca agtccatttc aatgatggc 360
158 tatggcaagg agcatggcg tatttgc当地ggg acatgttccg gctt当地ttaat 420
159 gaactgc当地ga aggacaagaa cctcacttgc accglocaltcaag tt当地tctactt ggaaatttac 480
160 aatgaacgag tgc当地gactt gctgaatccg tgc当地caagg ggaatctcaa ggtcc当地gagaa 540
161 caccgc当地ga cc当地ccctta cgttccggagc tt当地gaaggc tt当地tctgtc当地g atc当地tccaa 600
162 gaaatcgaaa atctcatgta tgaggcgcaac aaagccagaa cc当地tccgc当地c caca当地acatg 660
163 aacgagacat cc当地tgc当地tccacccgtc tt当地acttgc当地t cttgacgc当地a aaagttggcat 720
164 gatgaagaga cccaaatgga cacagagaag gttgcaaga tcaatgc当地tgtt agatgttggc 780
165 ggttctgago gagcaacgctc caccggagct actggagc当地g gactgaaagg ggtt当地cagag 840
166 atcaaccgct cacttgc当地tccatggcgt gt当地tgc当地g cgcttagc当地g tatgtc当地tgc 900
167 ggaaaacaga agaagaatca gtttagtacct taccgagatt cggtaactgac gtggcttctg 960
168 aaggactcct tgggaggc当地a ctc当地atgacc gccatgatttccg cc当地tccatttc gc当地tctgtat 1020
169 attaactttg aagagactt cagtaaccctt cgtatgc当地gg actctgc当地aa gc当地aatcaag 1080
170 aaccacgc当地g tggtaatgta agacccgaaac gc当地cgatgta tccgc当地gaggaa 1140
171 ct当地cgcc当地g tgaggagcaaa actccagagc agtggg当地ggag gtggagggtgg tgc当地aggaggt 1200
172 tctggccggc当地g cagtgaggaa atc当地taccctt cccgacacgc当地c cgctcgagaa gcaatc当地gtg 1260
173 tc当地attc当地g agccggatgc gacagtcaag aaaatgagca aggc当地gaaat cgtggagc当地a 1320
174 ct当地aacc当地g agtggaaagct ctatcggtt当地tcaatc当地gaa cctggg当地aaga gaagctggcc 1380
175 aagaccgagg aaatccaccaa ggaacgagaa gc当地ggc当地tgc当地g aggagctggg tatc当地agcatc 1440
176 gaaaagggct tt当地tggccc tt当地accacttca aaagaaatgc当地c cacaatctgtt caacttgc当地g 1500
177 gatgatc当地tcc tt当地tggctgta gt当地tcttgc当地tacaacatca agccccc当地gca gacaagggtt 1560
178 ggaaacgtca accaagatac acaacgagaa attc当地tctgta acggg当地tgc当地aa gatc当地tgc当地aa 1620
179 gaacactgta cgtt当地gaaaa tggtaacac gttgtaacttca tctgtaacttca cggagggct 1680
180 gctgtcatgg tgaacglocaltgc当地g gcaatc当地gac aagccctacttccg cc当地tcccg当地g cggctacagg 1740
181 atc当地atc当地tccg localtgc当地tccatggta tt当地accatc当地tccg cc当地tccg当地gaa 1800
182 cggcaagaac aatc当地tctgct tc当地ccatttctt gtc当地accatca gtc当地gttggg tt当地ccctgct 1860
183 cc当地aggcc当地tcc acgaccggac actgagcaag gc当地ggg当地tccg atgccggacgg cgatc当地tccg 1920
184 tc当地agatttcc tt当地tccgca tt当地tctgtgta aaggatagc当地tcttccg cc当地tcccg当地gagg 1980
185 gaagctgcttca ggc当地gatc当地tcc aggggttggat cagaagatct ct当地atctgac当地tccg agatgacgag 2040
186 tt当地ggatgcat tatttgc当地tca tggtaacttca ggc当地ggg当地tccg tt当地tctgtgta gctgggtggaa 2100
187 gacaacgagaa atagc当地tcc gcaacttccg tt当地ccctgcttccg gt当地acaata catgtaat 2160
188 ggaaccatttgc当地tcc gtc当地gatacc gcaacttccg tt当地ccctgcttccg gt当地acaata catgtaat 2220
189 gatgacgacg gtc当地gatcc gttt当地tggat gataagaatg cggaaacgagaa tgc当地gttccat 2280
190 gttgatgttgc当地tcc tcaacagc当地gac gtc当地agatgg aagaaggccctt gaaaacagc当地g 2340
191 aagc当地aggat tc 2352
193 <210> SEQ ID NO: 3
194 <211> LENGTH: 21
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence

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197 <220> FEATURE:  
198 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
199 <400> SEQUENCE: 3  
200 atgtcgggcg gtggaaatat c 21  
202 <210> SEQ ID NO: 4  
203 <211> LENGTH: 23  
204 <212> TYPE: DNA  
205 <213> ORGANISM: Artificial Sequence  
206 <220> FEATURE:  
207 <223> OTHER INFORMATION: Description of Artificial Sequence:primer  
208 <400> SEQUENCE: 4  
209 gaattccctgc ttgcgtgttt tca 23  
211 <210> SEQ ID NO: 5  
212 <211> LENGTH: 30  
213 <212> TYPE: DNA  
214 <213> ORGANISM: Artificial Sequence  
215 <220> FEATURE:  
216 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate  
forward primer  
217 <220> FEATURE:  
219 <221> NAME/KEY: modified\_base  
220 <222> LOCATION: (25)  
221 <223> OTHER INFORMATION: n = a, c, g or t  
222 <400> SEQUENCE: 5  
W--> 223 ggcgcggatcc atytytgcht ayggncarac 30  
225 <210> SEQ ID NO: 6  
226 <211> LENGTH: 30  
227 <212> TYPE: DNA  
228 <213> ORGANISM: Artificial Sequence  
229 <220> FEATURE:  
230 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate  
reverse primer  
231 <220> FEATURE:  
233 <221> NAME/KEY: modified\_base  
234 <222> LOCATION: (16)  
235 <223> OTHER INFORMATION: n = a, c, g or t  
236 <220> FEATURE:  
237 <221> NAME/KEY: modified\_base  
238 <222> LOCATION: (28)  
239 <223> OTHER INFORMATION: n = a, c, g or t  
240 <400> SEQUENCE: 6  
W--> 241 gcgcaattc tcdganccdg cvarrtcnac 30  
243 <210> SEQ ID NO: 7  
244 <211> LENGTH: 30  
245 <212> TYPE: DNA  
246 <213> ORGANISM: Artificial Sequence  
247 <220> FEATURE:  
248 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate  
reverse primer

RAW SEQUENCE LISTING ERROR SUMMARY                   DATE: 09/04/2002  
PATENT APPLICATION: US/09/724,586                   TIME: 11:57:36

Input Set : N:\Crf3\RULE60\09724586.raw  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 25  
Seq#:6; N Pos. 16,28  
Seq#:7; N Pos. 16,28

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VERIFICATION SUMMARY  
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Input Set : N:\Crf3\RULE60\09724586.raw  
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L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0